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<110> Yanofsky, Martin F.

The Regents of the University of California

<120> Methods of Suppressing Flowering in Transgenic Plants

<130> 19452A-002210US

<140> US 09/869,582

<141> 2002-02-28

<150> US 60/104,604

<151> 1998-10-16

<150> WO PCT/US99/24407

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<170> PatentIn Ver. 2.1

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Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu						
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tgc gat gct gaa gtc tct ctc atc gtc ttc tcc aac cgt ggc aag ctc	500					
Cys Asp Ala Glu Val Ser Leu Ile Val Phe Ser Asn Arg Gly Lys Leu						
	40			45		50
tac gag ttc tgc agc acc tcc aac atg ctc aag aca ctg gaa agg tat	548					
Tyr Glu Phe Cys Ser Thr Ser Asn Met Leu Lys Thr Leu Glu Arg Tyr						
	55			60		65
cag aag tgt agc tat ggc tcc att gaa gtc aac aac aaa cct gct aaa	596					
Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val Asn Asn Lys Pro Ala Lys						
	75			80		85
gag ctt gag aac agc tac aga gag tac ttg aag ctg aaa ggt aga tat	644					
Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu Lys Leu Lys Gly Arg Tyr						
	90			95		100
gaa aat ctg caa cgt cag cag aga aat ctt ctt gga gag gat ctt gga	692					
Glu Asn Leu Gln Arg Gln Gln Arg Asn Leu Leu Gly Glu Asp Leu Gly						
	105			110		115
cct ctg aat tca aag gag cta gag cag ctt gag cgt caa cta gac ggc	740					
Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu Glu Arg Gln Leu Asp Gly						
	120			125		130
tct ctg aag caa gtt cgc tgc atc aag aca cag tat atg ctt gac cag	788					
Ser Leu Lys Gln Val Arg Cys Ile Lys Thr Gln Tyr Met Leu Asp Gln						
	135			140		145
ctc tct gat ctt caa ggt aag gag cat atc ttg ctt gat gcc aac aga	836					
Leu Ser Asp Leu Gln Gly Lys Glu His Ile Leu Leu Asp Ala Asn Arg						
	155			160		165
gct ttg tca atg aag ctg gaa gat atg atc ggc gtg aga cat cac cat	884					
Ala Leu Ser Met Lys Leu Glu Asp Met Ile Gly Val Arg His His His						
	170			175		180
ata gga gga gga tgg gaa ggt ggt gat caa cag aat att gcc tat gga	932					
Ile Gly Gly Gly Trp Glu Gly Gly Asp Gln Gln Asn Ile Ala Tyr Gly						
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cat cct cag gct cat tct cag gga cta tac caa tct ctt gaa tgt gat	980					
His Pro Gln Ala His Ser Gln Gly Leu Tyr Gln Ser Leu Glu Cys Asp						
	200			205		210

ccc act ttg caa att gga tat agc cat cca gtg tgc tca gag caa atg 1028
 Pro Thr Leu Gln Ile Gly Tyr Ser His Pro Val Cys Ser Glu Gln Met
 215 220 225 230

gct gtg acg gtg caa ggt cag tcc caa caa gga aac ggc tac atc cct 1076
 Ala Val Thr Val Gln Gly Gln Ser Gln Gln Gly Asn Gly Tyr Ile Pro
 235 240 245

ggc tgg atg ctg tga gcgatacttc ttccccaat aaagatctta agcaagtact 1131
 Gly Trp Met Leu
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aagacttttg cttttgtaga cacaagtggc tatagctgta atagccttca acatctctct 1251

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 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ser Leu Ile Val Phe
 35 40 45
 Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Thr Ser Asn Met Leu
 50 55 60
 Lys Thr Leu Glu Arg Tyr Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val
 65 70 75 80
 Asn Asn Lys Pro Ala Lys Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu
 85 90 95
 Lys Leu Lys Gly Arg Tyr Glu Asn Leu Gln Arg Gln Gln Arg Asn Leu
 100 105 110
 Leu Gly Glu Asp Leu Gly Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu
 115 120 125
 Glu Arg Gln Leu Asp Gly Ser Leu Lys Gln Val Arg Cys Ile Lys Thr
 130 135 140
 Gln Tyr Met Leu Asp Gln Leu Ser Asp Leu Gln Gly Lys Glu His Ile
 145 150 155 160
 Leu Leu Asp Ala Asn Arg Ala Leu Ser Met Lys Leu Glu Asp Met Ile
 165 170 175
 Gly Val Arg His His His Ile Gly Gly Gly Trp Glu Gly Gly Asp Gln
 180 185 190
 Gln Asn Ile Ala Tyr Gly His Pro Gln Ala His Ser Gln Gly Leu Tyr
 195 200 205
 Gln Ser Leu Glu Cys Asp Pro Thr Leu Gln Ile Gly Tyr Ser His Pro
 210 215 220

Val	Cys	Ser	Glu	Gln	Met	Ala	Val	Thr	Val	Gln	Gly	Gln	Ser	Gln	Gln
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<223> AGAMOUS-LIKE 9 (AGL9)
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Lys Ile Asn Arg Gln Val Thr Phe Ala Lys Arg Arg Asn Gly Leu Leu
15 20 25 30

aag aaa gca tac gag ctt tca gtt cta tgt gat gcg gaa gtt gct ctc 147
Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu
35 40 45

atc atc ttc tca aat aga gga aag ctg tac gag ttt tgc agt agt tcg 195
Ile Ile Phe Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Ser Ser
50 55 60

agc atg ctt cgg aca ctg gag agg tac caa aag tgt aac tat gga gca 243
Ser Met Leu Arg Thr Leu Glu Arg Tyr Gln Lys Cys Asn Tyr Gly Ala

65 70 75

cca gaa ccc aat gtg cct tca aga gag gcc tta gca gaa ctt agt agc 291
Pro Glu Pro Asn Val Pro Ser Arg Glu Ala Leu Ala Glu Leu Ser Ser
80 85 90

cag cag gag tat ctc aag ctt aag gag cgt tat gac gcc tta cag aga 339
Gln Gln Glu Tyr Leu Lys Leu Lys Glu Arg Tyr Asp Ala Leu Gln Arg
95 100 105 110

acc caa agg aat ctg ttg gga gaa gat ctt gga cct cta agt aca aag 387
Thr Gln Arg Asn Leu Leu Gly Glu Asp Leu Gly Pro Leu Ser Thr Lys
115 120 125

gag ctt gag tca ctt gag aga cag ctt gat tct tcc ttg aag cag atc 435
Glu Leu Glu Ser Leu Glu Arg Gln Leu Asp Ser Ser Leu Lys Gln Ile
130 135 140

aga gct ctc agg aca cag ttt atg ctt gac cag ctc aac gat ctt cag 483
Arg Ala Leu Arg Thr Gln Phe Met Leu Asp Gln Leu Asn Asp Leu Gln
145 150 155

agt aag gaa cgc atg ctg act gag aca aat aaa act cta aga cta agg	531
Ser Lys Glu Arg Met Leu Thr Glu Thr Asn Lys Thr Leu Arg Leu Arg	
160 165 170	
tta gct gat ggg tat cag atg cca ctc cag ctg aac cct aac caa gaa	579
Leu Ala Asp Gly Tyr Gln Met Pro Leu Gln Leu Asn Pro Asn Gln Glu	
175 180 185 190	
gag gtt gat cac tac ggt cgt cat cat cat caa caa caa caa cac tcc	627
Glu Val Asp His Tyr Gly Arg His His His Gln Gln Gln Gln His Ser	
195 200 205	
caa gct ttc ttc cag cct ttg gaa tgt gaa ccc att ctt cag atc ggg	675
Gln Ala Phe Phe Gln Pro Leu Glu Cys Glu Pro Ile Leu Gln Ile Gly	
210 215 220	
tat cag ggg caa caa gat gga atg gga gca gga cca agt gtg aat aat	723
Tyr Gln Gly Gln Gln Asp Gly Met Gly Ala Gly Pro Ser Val Asn Asn	
225 230 235	
tac atg ttg ggt tgg tta cct tat gac acc aac tct att tga atc ttt	771
Tyr Met Leu Gly Trp Leu Pro Tyr Asp Thr Asn Ser Ile Ile Phe	
240 245 250	
ctc act taa tca atc cct ctc ttt ttt ttt ttg aca ttt tta aga tga	819
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<211> 251

<212> PRT

<213> Arabidopsis thaliana

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Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Ile	
35 40 45	
Phe Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Ser Ser Ser Met	
50 55 60	
Leu Arg Thr Leu Glu Arg Tyr Gln Lys Cys Asn Tyr Gly Ala Pro Glu	
65 70 75 80	
Pro Asn Val Pro Ser Arg Glu Ala Leu Ala Glu Leu Ser Ser Gln Gln	
85 90 95	
Glu Tyr Leu Lys Leu Lys Glu Arg Tyr Asp Ala Leu Gln Arg Thr Gln	
100 105 110	
Arg Asn Leu Leu Gly Glu Asp Leu Gly Pro Leu Ser Thr Lys Glu Leu	
115 120 125	
Glu Ser Leu Glu Arg Gln Leu Asp Ser Ser Leu Lys Gln Ile Arg Ala	
130 135 140	
Leu Arg Thr Gln Phe Met Leu Asp Gln Leu Asn Asp Leu Gln Ser Lys	
145 150 155 160	

Glu	Arg	Met	Leu	Thr	Glu	Thr	Asn	Lys	Thr	Leu	Arg	Leu	Arg	Leu	Ala
			165						170					175	
Asp	Gly	Tyr	Gln	Met	Pro	Leu	Gln	Leu	Asn	Pro	Asn	Gln	Glu	Glu	Val
			180					185					190		
Asp	His	Tyr	Gly	Arg	His	His	His	Gln	Gln	Gln	Gln	His	Ser	Gln	Ala
		195					200					205			
Phe	Phe	Gln	Pro	Leu	Glu	Cys	Glu	Pro	Ile	Leu	Gln	Ile	Gly	Tyr	Gln
	210					215					220				
Gly	Gln	Gln	Asp	Gly	Met	Gly	Ala	Gly	Pro	Ser	Val	Asn	Asn	Tyr	Met
225					230					235					240
Leu	Gly	Trp	Leu	Pro	Tyr	Asp	Thr	Asn	Ser	Ile					
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 gattttacta tattacaatt ttttcttttt acatggtcta atttattttt ctaaaattag 360
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Met Gly Arg Gly Arg Val Gln Leu Lys Arg Ile
      1              5              10

gag aac aag atc aat aga caa gtg aca ttc tcg aaa aga aga gct ggt 221
Glu Asn Lys Ile Asn Arg Gln Val Thr Phe Ser Lys Arg Arg Ala Gly
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Leu Leu Lys Lys Ala His Glu Ile Ser Val Leu Cys Asp Ala Glu Val
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gct ctt gtt gtc ttc tcc cat aag ggg aaa ctc ttc gaa tac tcc act 317
Ala Leu Val Val Phe Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Thr
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gat tct tgt atg gag aag ata ctt gaa cgc tat gag agg tac tct tac 365
Asp Ser Cys Met Glu Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr
      60              65              70              75

gcc gaa aga cag ctt att gca cct gag tcc gac gtc aat aca aac tgg 413
Ala Glu Arg Gln Leu Ile Ala Pro Glu Ser Asp Val Asn Thr Asn Trp
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Asn Gln Arg His Tyr Leu Gly Glu Asp Leu Gln Ala Met Ser Pro Lys
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Glu Leu Gln Asn Leu Glu Gln Gln Leu Asp Thr Ala Leu Lys His Ile
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cgc act aga aaa aac caa ctt atg tac gag tcc atc aat gag ctc caa 605
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Ile Lys Glu Arg Glu Lys Ile Leu Arg Ala Gln Gln Glu Gln Trp Asp
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Gln Gln Asn Gln Gly His Asn Met Pro Pro Pro Leu Pro Pro Gln Gln
          190                      195                      200

cac caa atc cag cat cct tac atg ctc tct cat cag cca tct cct ttt 797
His Gln Ile Gln His Pro Tyr Met Leu Ser His Gln Pro Ser Pro Phe
          205                      210                      215

ctc aac atg ggt ggt ctg tat caa gaa gat gat cca atg gca atg agg 845
Leu Asn Met Gly Gly Leu Tyr Gln Glu Asp Asp Pro Met Ala Met Arg
          220                      225                      230                      235

agg aat gat ctc gaa ctg act ctt gaa ccc gtt tac aac tgc aac ctt 893
Arg Asn Asp Leu Glu Leu Thr Leu Glu Pro Val Tyr Asn Cys Asn Leu
          240                      245                      250

ggc tgc ttc gcc gca tga agcatttcca tatatatata tttgtaatcg 941
Gly Cys Phe Ala Ala
          255

tcaacaataa aaacagtttg ccacatacat ataaatagtg gctaggctct tttcatccaa 1001

ttaatatatt ttggcaaagtttgcgatgttc ttatatcatc atatataaat tagcaggctc 1061

ctttcttctt ttgtaatttg ataagtttat ttgcttcaat atggagcaaa attgtaatat 1121

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<211> 256

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> AP1

<400> 14

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His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Val Phe
          35           40           45
Ser His Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu
          50           55           60
Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Arg Gln Leu
          65           70           75           80
Ile Ala Pro Glu Ser Asp Val Asn Thr Asn Trp Ser Met Glu Tyr Asn
          85           90           95
Arg Leu Lys Ala Lys Ile Glu Leu Leu Glu Arg Asn Gln Arg His Tyr
          100          105          110
Leu Gly Glu Asp Leu Gln Ala Met Ser Pro Lys Glu Leu Gln Asn Leu
          115          120          125
Glu Gln Gln Leu Asp Thr Ala Leu Lys His Ile Arg Thr Arg Lys Asn
          130          135          140
Gln Leu Met Tyr Glu Ser Ile Asn Glu Leu Gln Lys Lys Glu Lys Ala
          145          150          155          160
Ile Gln Glu Gln Asn Ser Met Leu Ser Lys Gln Ile Lys Glu Arg Glu
          165          170          175
Lys Ile Leu Arg Ala Gln Gln Glu Gln Trp Asp Gln Gln Asn Gln Gly
          180          185          190
His Asn Met Pro Pro Pro Leu Pro Pro Gln Gln His Gln Ile Gln His
          195          200          205
Pro Tyr Met Leu Ser His Gln Pro Ser Pro Phe Leu Asn Met Gly Gly
          210          215          220
Leu Tyr Gln Glu Asp Asp Pro Met Ala Met Arg Arg Asn Asp Leu Glu
          225          230          235          240
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<211> 1374

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

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<400> 15

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aagaaagcta attaaagttt tctctctagc tattctctct cttttcttgt tcttgaaaac 180
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tataaaagag ggaaaataag ataggggatt tttgggggtg ggaaagatgg gaagaggaag 360
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<210> 16
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<213> Arabidopsis thaliana

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<220>
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<220>
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<223> AGL2

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aaaagaatca ataaccctat aaataaaaaa tcagacaaac agaagtttcc tcttcttctt 180
ccttaagcta gtaccttttg ttcttgaaat taggggttaat ttcttttttc caaataccat 240
caatttctca gaccataaaa actcaaaaag atcagatctt tcctctgaaa aagagatacc 300
caacttatgt ttttgtgtgt ctgtatatag ataaacatta catacccata tttgtgtata 360
gacataaaaa gtggaaatta aggtaacaaa aagaaatggg aagaggaaga gtagagctga 420
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<223> Description of Artificial Sequence:forward primer
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<400> 17

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30

<210> 18

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:reverse primer
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<400> 18

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28